

FIGURE 1

GCTCTCCCTGCTCCAGCAAGGACCATGAGGGCGCTGGAGGGGCCAGGCCTGTCGCTGCTG
M R A L E G P G L S L L

TGCCTGGTGTGGCGCTGCCTGCCCTGCTGCCGGTGCCGGCTGTACGCGGAGTGGCAGAA
C L V L A L P A L L P V P A V R G V A E

ACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCAGTGC
T P T Y P W R D A E T G E R L V C A Q C

CCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCG
P P G T F V Q R P C R R D S P T T C G P

TGTCCACCGCGCCACTACACGCAGTTCTGGAACCTGAGAGCGCTGCCGCTACTGCAAC
C P P R H Y T Q F W N Y L E R C R Y C N

GTCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCC
V L C G E R E E E A R A C H A T H N R A

TGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGT
C R C R T G F F A H A G F C L E H A S C

CCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCG
P P G A G V I A P G T P S Q N T Q C Q P

TGCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGC
C P P G T F S A S S S S S E Q C Q P H R

AACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTG
N C T A L G L A L N V P G S S S H D T L

TGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
C T S C T G F P L S T R V P G A E E C E

CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTG
R A V I D F V A F Q D I S I K R L Q R L

CTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGCCGCGGGCC
L Q A L E A P E G W G P T P R A G R A A

TTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTG
L Q L K L R R R L T E L L G A Q D G A L

CTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCCGGGCTGGAGCGGAGCGTC
L V R L L Q A L R V A R M P G L E R S V

CGTGAGCGCTTCCTCCCTGTGCACTGATCCTGGCCCCCTCTTATTTATTCTACATCCTTG
R E R F L P V H *

GCACCCCACTTGCACTGAAAGAGGCTTTTTTTTAAATAGAAGAAATGAGGTTTCTTAAAG
CTTATTTTATAAAGCTTTTTCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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TGGCATGTCGGTCAGGCACAGCAGGGTCTCTGTGTCCGCGCTGAGCCGCGCTCTCCCTGCCT
CCAGCAAGGACCATGAGGGCGCTGGAGGGGCCAGGCCTGTGCTGCTGTGCCTGGTGTGTG
M R A L E G P G L S L L C L V L
CGCTGCCTGCCCTGCTGCCGGTGCCGGCTGTACGCGGAGTGGCAGAAACACCCACCTAC
A L P A L L P V P A V R G V A E T P T Y
CCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCAGTGCCCCCAGGCACC
P W R D A E T G E R L V C A Q C P P G T
TTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGC
F V Q R P C R R D S P T T C G P C P P R
CACTACACGCAGTTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGG
H Y T Q F W N Y L E R C R Y C N V L C G
GAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGC
E R E E E A R A C H A T H N R A C R C R
ACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGAGCACGCATCGTGTCCACCTGGTGCC
T G F F A H A G F C L E H A S C P P G A
GGCGTGATTGCCCCGGGTGAGAGCTGGGCGAGGGGAGGGGCCCCCAGGAGTGGTGCCGG
G V I A P G E S W A R G G A P R S G G R
AGGTGTGGCAGGGGTCAGGTTGCTGGTCCCAGCCTTGACCCCTGAGCTAGGACACCAGTT
R C G R G Q V A G P S L A P *
CCCCTGACCCTGTTCTTCCCTCCTGGCTGCAGGCACCCCCAGCCAGAACACGCAGTGCCA
GCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCA
CCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACAC
CCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGTGAGCCAGAGGC
CTGAGGGGGCAGCACACTGCAGGCCAGGCCCACTTGTGCCCTCACTCCTGCCCTGCACG
TGCATCTAGCCTGAGGCATGCCAGCTGGCTCTGGGAAGGGGCCACAGTGGATTTGAGGGG
TCAGGGGTCCCTCCACTAGATCCCCACCAAGTCTGCCCTCTCAGGGGTGGCTGAGAATTT
GGATCTGAGCCAGGGCACAGCCTCCCCTGGAGAGCTCTGGGAAAGTGGGCAGCÀATCTCC

FIGURE 2 (continued)

TAACTGCCCCGAGGGGAAGGTGGCTGGCTCCTCTGACACGGGGAAACCGAGGCCTGATGGT
AACTCTCCTAACTGCCTGAGAGGAAGGTGGCTGCCTCCTCTGACATGGGGAAACCGAGGC
CCAATGTTAACCACTGTTGAGAAGTCACAGGGGGAAGTGACCCCTTAACATCAAGTCAG
GTCCGGTCCATCTGCAGGTCCCAACTCGCCCTTCCGATGGCCCAGGAGCCCCAAGCCCT
TGCCTGGGCCCCCTTGCTCTTGACAGCAAGGTCCGAGTGGCCGCTCCTGCCCCCTAGGC
CTTTGCTCCAGCTCTCTGACCGAAGGCTCCTGCCCCCTTCTCCAGTCCCCATCGTTGCACT
GCCCCCTCCAGCACGGCTCACTGCACAGGGATTTCTCTCTCCTGCAAACCCCCGAGTGG
GGCCCAGAAAGCAGGGTACCTGGCAGCCCCCGCCAGTGTGTGTGGGTGAAATGATCGGAC
CGCTGCCTCCCCACCCCACTGCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTG
TGGCTTTCCAGGACATCTCCATCAAGAGGAGCGGCTGCTGCAGGCCC

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FIGURE 3

1 M-GTSTVPDLLLPVLLELVGIVPSGVIGLVPHLGDR- INR1
1 MAPVAVWALAVGLELWAAAHAPQA- - - - -FTP- - - - - INR2
1 MGAGATGRAND- - - - -GRLDLLLHGLVSLGAK-ACP- - - - - INR
1 M-RTPR-ASSPCGLWAGPVLLEGLSGELVASQPOLVP- - - - - INR
1 MLCIMT- - - - -LPLTTSV-ARLSSKSVNAQVTDINSKGL INR
1 M- - - - -ARPH- - - - -WLCVLGLTGLS-ATPAPKSCP- - - - - INR
1 MRLP- - - - -CUL- - - - -LALGLLFLGALRA- - - - -FPO- - - - - INR
1 MGN- - - - -SCYNIVATLVLVLN- - - - -TAVHPE- - - - -FER- - - - - INR
1 MCVGA- - - - -RLG- - - - -RGPALLLGLGLSTVGLHCY- - - - - INR
1 MKSV-LYLYI- - - - -LFLSSCIINGRDAAP- - - - -YTP- - - - - INR
1 MKS- - - - -YILL- - - - -LFLSSCIINGRDAAP- - - - -YTP- - - - - INR
1 MRALE- - - - -GPGLSLGLTGLVLPALP- - - - -VPA- - - - - INR-6A
1 MRALE- - - - -GPGLSLGLTGLVLPALP- - - - -VPA- - - - - INR-6B

27 -VARGVAETPTYPWRDA-ETGERLVCAQCPCPGTFVQRP- - - - - INR-6A
27 -VARGVAETPTYPWRDA-ETGERLVCAQCPCPGTFVQRP- - - - - INR-6B

75 P-GGDDTDCR-ECESGS-FTASENHLRHCLSCSK-CKREHG INR1
75 TKTSDTVC-DSC-EDSTYTOILMNWVECLSCGSRCSDDQV INR2
75 NO-T-V-CE-PCLDSTVTFSDVVSATEPCPKCT-ECVGLDS INR
75 SRSQDTCV-KTC-PHNSYNEHNLHSTCULCRP-CDIVLGL INR
75 N-GDEPDGV-PCOEGEKETDKAHFSSKCRRCRL-CEDEHG INR
75 HRKA-AQC-D-PCIPGVSSP- - - - - INR
75 R-PTDCRKC-EPDYXLDADRCTACVTGS- - - - -RD INR
75 TEFTETEC-LPC-GESEFLDWNRETCHQHXY-CDPMLG INR
75 NRNO- - - - -I-SPC-PPNSFSSA-GGORTCDICR-OC- - - - -KG 4-1B
75 SONT-V-CR-PC-GGFLYNDVSSK-PCKPCT-WC-NLRS INR
75 KNTNT-OC-TPC-GSGTFTSRNNHLPACTLSCNCRCDNSNOV INR
75 KNTNT-OC-TPC-ASDFTSRNNHLPACTLSCNCRCDNSNOV INR

67 RDSPTTC-GPC-PPRHYTOFWNYLERCRYCNVLCGEREE INR-6A
67 RDSPTTC-GPC-PPRHYTOFWNYLERCRYCNVLCGEREE INR-6B

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264	T K P L A F N P S F S G T P T G C F T P T L G F S P V H J S S T F T S S T Y T P G D	INR1
294	- - - - - L O R E A K V N S H L P A - D K A R G T Q G P E Q U H L I T A -	INR2
281	- - - - - N K O G A N S R L P A - N O T P P B E G E K L H S D G I S V D	NBR
262	- - - - - P E G E S P C P A - P R A D P H F P D L A E P L -	LHR
212	- - - - - S P T L N P E - - T V A I N L S D V D L S K Y I T T -	FSS
169	- - - - - T F E A P P L G T O P D C N P T P E - N G E A P A S T S P T Q S L V D S Q A	LP CD07
322	- - - - - P T N K A P H P K Q E - P Q - E I N F P D -	CD10
222	- - - - - T S Q G P S T R P V - E - V P G G R A V A A I L G L G L -	4-1BB
193	- - - - - L N F E I K C M N - - - - - K G S - S F K Q -	CD10
255	- - - - - L N F E I K C M N - - - - - K D S Y S S S K Q -	VC22
229	- - - - - L Q R L Q A L E A P E - G W - G P -	INR-6A
143	- - - - - E - S W A R G G -	INR-6B
704	C P N F A A P P R E V A P P Y O G A D P I L A T A -	INR1
1	- - - - - P S S S S S L E S S A S A L -	INR2
505	S Q S L H D Q Q P H T Q T A S G Q A L K - -	NBR
506	- - - - - P M S G D L S P S P A G P P T -	LHR
171	A R T L S T H M P P Q R S L C S S D F I -	FSS
361	S K T L P I P T S A P V A L S S T G K P V L D A G P V L F W I L V L V V V G	CD10
241	- - - - - D L P G S N T A P V -	CD10
193	- - - - - A L T S T A L L F L -	4-1BB
224	- - - - - V L G L L -	CD10
274	- - - - - A K N D D G - M -	VC22
276	- - - - - T K N D D D S I -	CD10
246	- - - - - P R A G R A A L Q L K - - L -	INR-6A
151	- - - - - P R S G -	INR-6B
329	- - - - - L A S D P I P N P L Q K W E D S A H K P Q S L D T D D P A T L Y A V E	INR1
339	- - - - - D R R A P T R N Q P Q A P G V E A S G A G E A R A S T G S S D S	INR2
347	V E K L L -	NBR
303	- - - - - A P S L E E V L Q Q S P L - - - - - V Q A R E L -	LHR
240	- - - - - M T L S Q V -	FSS
207	G A L F L -	CD10
401	S S A F L C H R R A C R K R I R Q K L H L C Y P V Q T S Q P K L E L V D S R P	CD10
?	- - - - - Q E T L -	CD10
GRKKLL	- - - - -	4-1BB
281	- - - - - M S H S E T V T L A G D C L S S V D I Y I L Y S N T N	CD10
284	- - - - - M P H S E S V T L V G D C L S S V D I Y I L Y S N T N	CD10
258	- - - - - R R R T E L L G A Q D G A L L V R L L Q A L R -	INR-6A
155	- - - - -	INR-6B

INFR-6a
INFR-6b

FIGURE 3 (continued)

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365 NVPLRLWKEFVRRLGLSDHEIDRLLELQNGRCLREAYSM L TNR1
372 PGHGQTQVNVTCIVNVCCSSDH-SSQCSSQASTHGDT-- TNR2
385 AGDTWRHLA[GE]LGYPENID[SF]THEACPV- TNR2
397 PGEHQVAVH[GE]ANGIH[VT]GGSVTVTGNIVYNGPVLGGT-- LNR
404 ---KGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQL F5
411 RRSSTQLRS[GS]AS[VT]EPVAEERGLMSQPLMETCHSVGAAYL C27
426 ---H[GC]QPV- TNR2
435 ---RLPPD-AHKPP[GG]SF-- C27
448 AQDYETDTISYRVGNVLD[DS]HMPGSCNIHK-- 4-LIB
451 TQDYETDTISYHVGNNVLDVDSHMPGRCDTHK-- VC22
462 ---VARHP[GL]ER-- TNR-6a
475 ---GRCGRGQ-- TNR-6b

485 ATWRRTPRREATLELGRVLRDMDLGC-- TNR1
492 ASWATQDSATLDA-- QVPFSKECAF-- TNR2
509 ---RQPGDP-PAP--EPPYPTPEGA-- NER
521 RNMHQLHGKKEA-YDTLIKDLKANL--CTLAEKIQ-- LNR
538 ---EEGSTI-- F5
551 ESLPLQDASPAAG-PSSPRDLPEPRVSTEHTNKEIYI C27
568 --- C27
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607 --- C27
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633 --- C27
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09006352.011398

FIGURE 4

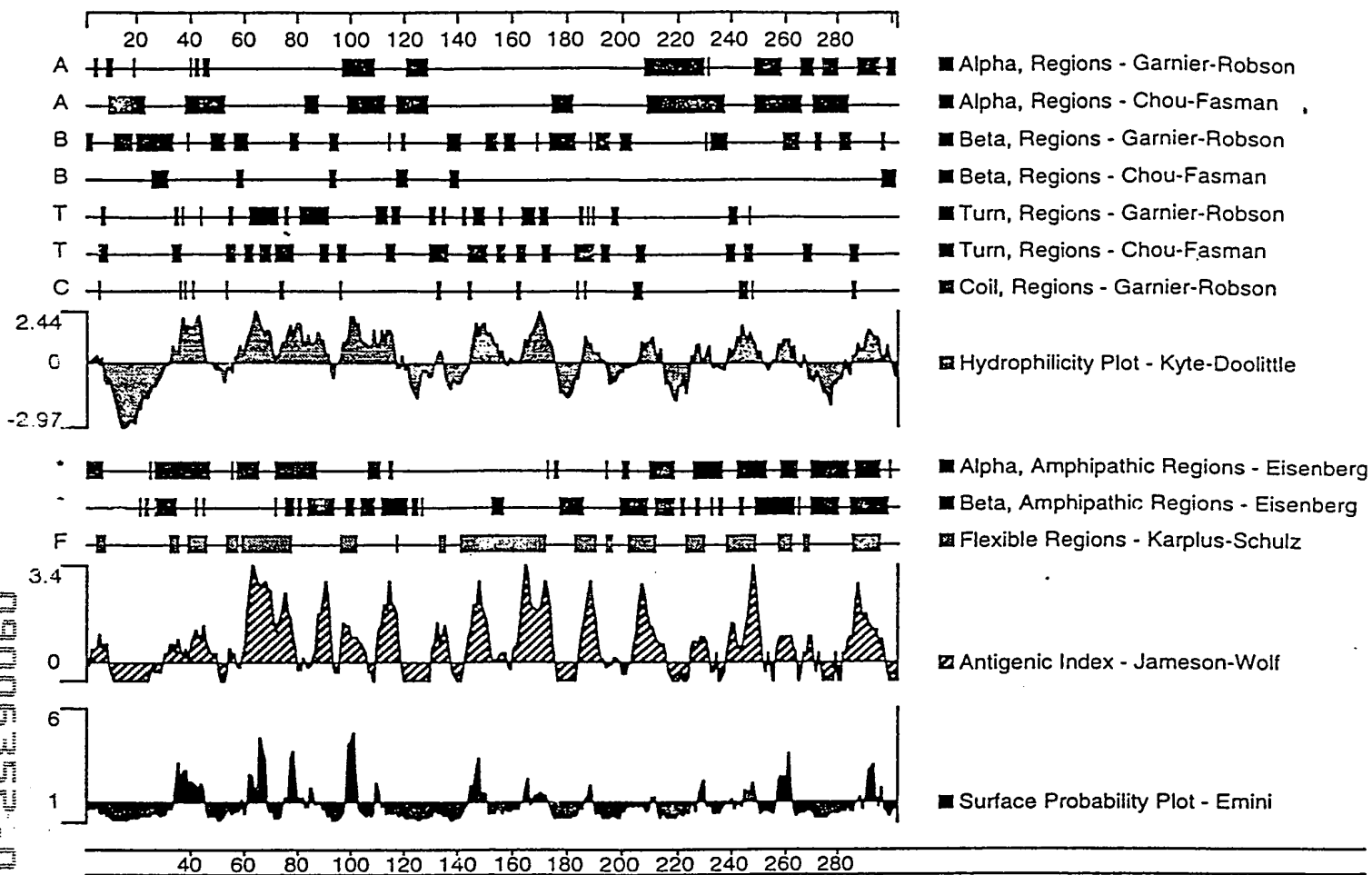


FIGURE 5

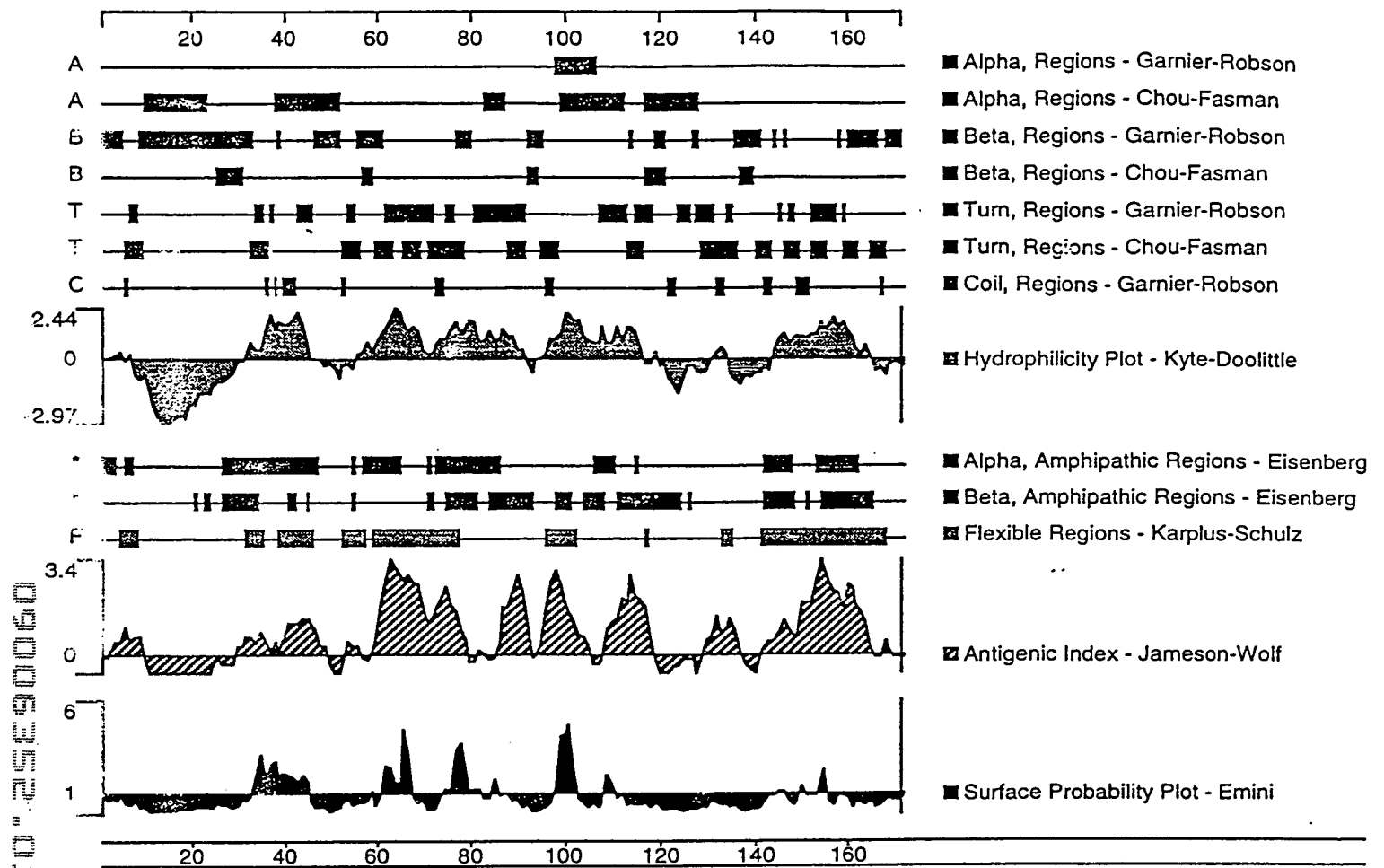


FIGURE 6

HELDI06R

GGCACGAGCA GGGTCCTGTN TCCGCCCTGA GCCGCGCTCT NCCTGCTCCA GCAAGGACCA
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TGCTGCCGGT GCCGGCTGTA CGCGGAGTGG CAGAAACACN NACNTACCCC TGGCGGGACG
NAGAGACAGG GGAGCGGCTG GTGTNTNCCC ANTGCCCCC AGGCACCTTT NTGCAGCGGC
CGTGCCGNCG AGACAGCCCC ACGACGTGTG GCGCGTNTCC ACCGCGCCAC TACACGCATT
CTGGAAC TAC CTGGAGCGCT GNCGTTACTN CAACGTCCTC TGCGGGGAGC GTNAGGAGGA
GGCACGGGTT TNCCACGNCA ACCACAACCG NGGNTTACCG TNGCCGNACC GGTTCCTTCG
NCGCAAGTTG GTTTTNNNTT TGGAGNAAGG ATTCGTGTTN CAATTNATTG ACGNAGTGAT
TNNNCNCGG AACTNAAA

HCEOW38R

CGCAACTGCA CGGCCCTGGG ACTGGCCCTC AATGTGCCAG GNTCTTCCTC CCATGACACC
CTGTGCACCA GCTGCACTGG CTTCCCCCTC AGCACCAGGG TACCANGAGC TGAGGAGTGT
GAGCNTGCCG TCATCGACTT TTTGGCTTTC CAGGACATCT CCATCAAGAG GCTGCAGCGG
CTGCTCANGC C

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